UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/604,926	08/27/2003	Itzhak Bentwich	06087.0200.CPUS07	1925

37808 7590 11/01/2006

ROSETTA-GENOMICS
c/o PSWS
700 W. 47TH STREET
SUITE 1000
KANSAS CITY, MO 64112

EXAMINER	
ZARA, JANE J	

ART UNIT	PAPER NUMBER
1635	

DATE MAILED: 11/01/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/604,926	BENTWICH, ITZHAK	
	Examiner	Art Unit	
	Jane Zara	1635	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *14 September 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *17-34* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *17-34* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *10-6-06, 10-6-06*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☒ Other: _____.

DETAILED ACTION

This Office action is in response to the communication filed 9-14-06.

Claims 17-34 are pending in the instant application.

Election/Restrictions

Applicant's election with traverse of Group I, original claims 1-10, 13, 14 and 16, and SEQ ID No. 1931, in the reply filed on 9-14-06 is acknowledged. The traversal is on the ground(s) that normally ten sequences constitute a reasonable number for examination absent exceptional cases and the examiner has failed to demonstrate that the claimed sequences are an exceptional case necessitating the number to be selected be less than ten. This is not found persuasive because the searches required for proper examination of more than one sequence would unduly burden the examiner. The MPEP at 803.04 provided guidance for the number of sequences that would optionally be examined. These guidelines were written, however, before the vast expansion of the sequences in the various data bases that now must be searched, such expansion due in part to the large amount of data generated from the various genome projects. Furthermore, the searches of the appropriate data bases required for one sequence would not necessarily be coextensive with the searches required for other sequences, although some overlap might occur.

The requirement is still deemed proper and is therefore made FINAL.

Original claims 1-16 have been canceled and replaced with new claims 17-34, and claims pertaining to Groups II and III are withdrawn from further

consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement with respect to single sequence requirements in the reply filed on 9-14-06.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 17-34 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In claim 17, line 5, and in claim 20, line 5, the term "at least 50/61" is vague and unclear. Appropriate clarification is required.

Claim 20 is not further limiting from claim 17, and claim 21 is not further limiting from claim 18, since both sets of claims encompass nucleic acids consisting of at least 18 nucleotides (e.g. of SEQ ID NO. 1931).

In claims 27 and 28, lines 1-2, the term "at least 15/19 complementary" is vague and unclear. Appropriate clarification is required.

In claims 33 and 34, line 1, the term "system" is vague and unclear. Appropriate clarification is required.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 17-34 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

No support has been found in the specification as originally filed for the ratio "50/61" recited in claims 17, 20, and for the ratio "15/19" recited in claims 27 and 28, nor has support been found for the size limitations of 18-120 nucleotides, or of 18-24 (e.g. as recited in claims 17, 19, 22 and 27). This is a new matter rejection. Applicant must point to support for these limitations in the original disclosure.

The claims are drawn to nucleic acids comprising SEQ ID No. 1931, SEQ ID No. 4539, and sequences that have approximately 80% identity with these SEQ ID Nos, or which polynucleotides share approximately 80% complementarity with a binding site of a target gene.

The specification and claims do not adequately describe the genus comprising polynucleotides with variable sequences (e.g. at least 80% identity) within SEQ ID Nos. 1931 or 4539, or which share 80% complementarity with a binding site of a target gene, or which are capable of modulating expression of any target gene. The claimed genus encompasses a broad array of nucleic acid molecules (thousands of sequences), and the disclosure fails to provide a

representative number of species for the broad genus and corresponding functions claimed, comprising variable sequences within 1931 or 4539, and capable of modulating expression of any target gene, or capable of binding an untranslated sequence of any target gene sharing at least 80% sequence identity.

The specification and claims do not adequately describe the concise structural features (e.g. the nucleotide sequences) that distinguish structures within each genus from those without. One of skill in the art would reasonably conclude that the disclosure fails to provide a representative number of species to describe the genus of molecules encompassed by the variable sequences claimed. Thus, one of skill in the art would reasonably conclude that Applicant was not in possession of this broadly claimed genus.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 17-34 are rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility.

The claims are drawn to probes, vectors and gene expression systems comprising polynucleotides between 18-120 nucleotides in length sharing at least 82% identity with SEQ ID No. 1931, or comprising at least 18 nucleotides of SEQ ID No. 4539.

Following the requirements of the Utility Guidelines (See Federal Register, Dec. 21, 1999, Vol. 64, No. 244, revised guidelines for Utility), the first inquiry is whether a credible utility is cited in the specification for use of the polynucleotides. The cited utilities in the specification are that the purportedly "novel" nucleic acids claimed are sequences that have not yet been found to exist in nature, but might exist, based on various assumptions and calculations made by Applicant. The specification describes (see *e.g.* figure 7) by schematic diagrams a "'genomically programmed cell-specific protein expression modulation concept of the conceptual model of the present invention." At paragraphs 103-104 of the instant specification, the theory behind generating these heretofore unidentified sequences is described: "A centerpiece of the present invention is a bioinformatics gene detection engine 100, which is a preferred implementation of a mechanism capable of bioinformatically detecting genes of the novel groups of genes of the present invention. ...it receives three types of input, expressed RNA data 102, expressed DNA data 104, and protein function data 106, performs a complex process of analysis of this data as elaborated below, and based on this analysis produces output of a bioinformatically detected group of novel genes designated 108." The instant disclosure teaches an approach, therefore, of using computer calculations to predict the possibility of sequences that might exist, but which sequences have not been identified in any biological system. A credible utility is assessed from the standpoint of whether a person of ordinary skill in the art would accept that the recited or disclosed invention is currently available for such use. Since the

polynucleotides claimed are sequences derived from a conceptual model, and have not been identified in any biological systems, the credible utility appears to be lacking.

The next issue is whether there are any well established or substantial utilities for the claimed polynucleotides. The instant sequences are computer-generated sequences that purportedly function in the regulation of expression of some heretofore unidentified target gene in some heretofore unidentified biological context (see *e.g.* fig 5 which illustrates a "'genomic records' concept of the conceptual model of the present invention, addressing the genomic differentiation enigma." See paragraph 0081 of the instant specification). No well established utilities for the claimed polynucleotides are identified in either the specification or in the prior art. The research contemplated by Applicant to characterize potential or purportedly naturally occurring polynucleotides that might act as intermediates in biological processes, does not constitute a specific and substantial utility. Identifying a possible polynucleotide sequence using computations or computer modeling does not define a "real world" context or use. Neither the specification as filed not any art of record discloses or suggests any property or activity for the nucleic acid compounds such that another non-asserted utility would be well established for these purported polynucleotides. There is no showing in the specification or the art that the polynucleotides claimed exist in any biological context, nor any showing of target gene binding, modulation or regulation.

Claims 17-34 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a credible, substantial or asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 17, 20, 31 and 32 are rejected under 35 U.S.C. 102(b) as being anticipated by Lanfranchi et al.

Lanfranchi et al teach an isolated nucleic acid consisting of 18-120 nucleotides comprising (or consisting of) at least 18 consecutive nucleotides of SEQ ID NO. 1931, or the complement thereof (see Accession No. F24424 and the accompanying alignment data of Lanfranchi et al and SEQ ID No. 1931).

Claims 17, 20, 31 and 32 are rejected under 35 U.S.C. 102(b) as being anticipated by NCI, CGAP.

NCI, CGAP teach an isolated nucleic acid consisting of 18-120 nucleotides comprising (or consisting of) at least 18 consecutive nucleotides of

SEQ ID NO. 1931, or the complement thereof (see Accession No. AW009266 and the accompanying alignment data of NCI, CGAP and SEQ ID No. 1931).

Conclusion

Certain papers related to this application may be submitted to Art Unit 1635 by facsimile transmission. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 C.F.R. ' 1.6(d)). The official fax telephone number for the Group is **571-273-8300**. NOTE: If Applicant *does* submit a paper by fax, the original signed copy should be retained by applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Jane Zara** whose telephone number is **(571) 272-0765.** If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Peter Paras, can be reached on (571) 272-4517. Any inquiry regarding this application should be directed to the patent analyst, Katrina Turner, whose telephone number is (571) 272-0564. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information

for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Jane Zara
10-25-06

J Zara TC 1600

JANE ZARA, PH.D.
PRIMARY EXAMINER

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:31:43 ; Search time 2388 Seconds
(without alignments)
1428.425 Million cell updates/sec

Title: US-10-604-926A-1931
Perfect score: 61
Sequence: 1 agctgccctcctcttctccc.....gggagaaggggtgggtgct 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 1484138

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		59	96.7	99	10	F24424	F24424 HSPD10720 H
c 2		43.4	71.1	83	7	AW009266	AW009266 ws80a06.x
3		27.6	45.2	77	9	DN374929	DN374929 LIB38529_
4		25.6	42.0	103	1	AA731471	AA731471 nz98f08.s
5		24.4	40.0	82	13	CW336527	CW336527 104_835_1
6		24.4	40.0	84	13	CW335786	CW335786 104_834_1
7		24.2	39.7	70	13	DU329889	DU329889 109848604
c 8		23.6	38.7	69	13	CW130949	CW130949 104_513_1
9		23.6	38.7	78	13	CW189398	CW189398 104_610_1
c 10		23.6	38.7	78	13	CW189398	CW189398 104_610_1
c 11		23.6	38.7	82	13	CW336527	CW336527 104_835_1
c 12		23.4	38.4	91	11	BH415834	BH415834 1007045A0
13		23.4	38.4	119	3	BP112776	BP112776 BP112776
14		23.2	38.0	55	9	DN373872	DN373872 LIB38528_
15		23.2	38.0	68	14	CR147982	CR147982 Forward_s
c 16		23	37.7	115	1	AI858529	AI858529 wl39h03.x
c 17		23	37.7	120	7	BE082457	BE082457 RC5-BT063
c 18		22.8	37.4	73	1	AI718969	AI718969 as50f01.x
19		22.8	37.4	98	5	CF197798	CF197798 maj40b02.
20		22.8	37.4	111	13	CW189218	CW189218 104_610_1
21		22.6	37.0	112	9	DN440660	DN440660 LIB5337-0
22		22.6	37.0	114	2	BF832254	BF832254 PM3-HT092
23		22.6	37.0	118	1	AI589396	AI589396 tr61h10.x
c 24		22.4	36.7	99	10	F24424	F24424 HSPD10720 H
c 25		22.4	36.7	117	12	CG566740	CG566740 OST192605
c 26		22.2	36.4	76	12	CG666867	CG666867 OST458079
c 27		22.2	36.4	98	13	CL279855	CL279855 Ggal_142c
c 28		22.2	36.4	107	8	CO529989	CO529989 3530_1_19
c 29		22.2	36.4	113	7	AW028147	AW028147 wv26f08.x
30		22.2	36.4	115	5	CD696564	CD696564 EST13087
c 31		22.2	36.4	119	1	AI824210	AI824210 wj36b05.x
32		22.2	36.4	119	14	CR001418	CR001418 Forward_s
33		22	36.1	70	14	DX107181	DX107181 644_2_141
c 34		22	36.1	70	14	DX107181	DX107181 644_2_141
35		22	36.1	72	14	CR194047	CR194047 Reverse_s
36		22	36.1	89	14	CR037539	CR037539 Reverse_s
37		22	36.1	94	8	CO887582	CO887582 BovGen_15
38		21.8	35.7	83	11	AZ639232	AZ639232 1M0499M06
39		21.8	35.7	110	5	CI299381	CI299381 CI299381
40		21.8	35.7	117	7	BE487605	BE487605 176447 BA
c 41		21.8	35.7	118	1	AA646954	AA646954 vn38d09.r
42		21.8	35.7	120	5	CI297065	CI297065 CI297065
43		21.6	35.4	101	5	CD945340	CD945340 RDX_27 Ge
44		21.6	35.4	101	8	CO824350	CO824350 LM_GB5_00
c 45		21.6	35.4	112	3	BU754334	BU754334 UI-1-BB1p

ALIGNMENTS

RESULT 1
F24424
LOCUS F24424 99 bp mRNA linear EST 13-MAY-1999
DEFINITION HSPD10720 HM3 Homo sapiens cDNA clone s4000009E12, mRNA sequence.
ACCESSION F24424
VERSION F24424.1 GI:4810050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 99)
AUTHORS Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
TITLE Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
JOURNAL Genome Res. 6 (1), 35-42 (1996)
PUBMED 8681137
COMMENT Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at http://grup.bio.unipd.it.
FEATURES Location/Qualifiers
source 1. .99
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="s4000009E12"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/clone_lib="HM3"
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI; Site_2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer (5'-biotin-AACCCGGCTCGAGCGGCCGCTTTTTTTTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range

350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector."
ORIGIN

Query Match 96.7%; Score 59; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGCCCTCCTCTTCTCCCCTCACACTACAGCCCTGGTGGGGGAGAAGGGGGTGGGTG 59
Db 41 AGCTGCCCTCCTCTTCTCCCCTCACACTACAGCCCTGGTGGGGGAGAAGGGGGTGGGTG 99

RESULT 2
AW009266/c
LOCUS AW009266 83 bp mRNA linear EST 08-MAR-2000
DEFINITION ws80a06.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504242 3', mRNA sequence.
ACCESSION AW009266
VERSION AW009266.1 GI:5858044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 83)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1204 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 82.
FEATURES Location/Qualifiers
source 1. .83
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2504242"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Co3"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. "
ORIGIN

Query Match 71.1%; Score 43.4; DB 7; Length 83;
Best Local Similarity 82.0%; Pred. No. 0.011;
Matches 50; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AGCTGCCCTCCTCTTCTCCCCTCACACTACAGCCCTGGTGGGGGAGAAGGGGGTGGGTGC 60
Db 65 AGCTGTCTTTTTTTTCTTCCTTTATACTACAGCTTTGGTGGGGGAGAAGGGGGTGGGTGC 6

Qy 61 T 61
Db 5 T 5

RESULT 3
DN374929
LOCUS DN374929 77 bp mRNA linear EST 07-MAR-2005
DEFINITION LIB38529_027_C11_T7_1 LIB38529 Canis familiaris cDNA clone LIB38529_027_C11, mRNA sequence.
ACCESSION DN374929
VERSION DN374929.1 GI:60556149
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 77)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
FEATURES Location/Qualifiers
source 1. .77
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="LIB38529_027_C11"
/tissue_type="heart"
/lab_host="DH10B"
/clone_lib="LIB38529"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI"
ORIGIN

Query Match 45.2%; Score 27.6; DB 9; Length 77;
Best Local Similarity 67.2%; Pred. No. 7.1e+02;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 3 CTGCCCTCCTCTTCTCCCCTCACACTACAGCCCTGGTGGGGGAGAAGGGGGTGGGTGC 60
Db 1 CCGCTCTCCTCTTCTCCCCCTCCCCCCCTTCCCGGGGGGCGGCGGAGGGCGGGGAGGC 58

RESULT 4
AA731471
LOCUS AA731471 103 bp mRNA linear EST 05-MAR-1998
DEFINITION nz98f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303527 3' similar to TR:O00146 O00146 P120E4F TRANSCRIPTION FACTOR. ;, mRNA sequence.
ACCESSION AA731471
VERSION AA731471.1 GI:2753627
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 103)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center